

2 32
CTT TCA GAA GCC CGG GAG AGC GTC TTG GGG GAT TTG CTG AAG GTT GTG CTG TAC AGC CTG
leu ser glu ala arg glu ser val leu gly asp leu leu lys val val leu tyr ser leu

62 92
GGC AGT GCC CAG AGT GCC CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG AGG GCC CTT GTG
gly ser ala gln ser ala leu phe leu gln his gly leu ala thr gln arg ala leu val

122 152
TCC AAG TTC CCG GAG CTG CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC GAC CTG TGC CTG
ser lys phe pro glu leu leu phe glu glu asp thr glu leu cys ala asp leu cys leu

182 212
AGG CTC CTA CGA CAC TGT GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC GCC AGC GCC TCG
arg leu leu arg his cys gly ser arg ile ser thr ile arg thr his ala ser ala ser

242 272
CTG TAC CTG CTC ATG CGA CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC CGT GTG AAG ATG
leu tyr leu leu met arg gln asn phe glu ile gly his asn phe ala arg val lys met

302 332
CAG GTC ACC ATG TCT CTC TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC AGT GAA GAG CAC
gln val thr met ser leu ser ser leu val gly thr thr gln asn phe ser glu glu his

362 392
CTG CGA CGT TCA CTC AAA ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG GGG CTG CGG GAC
leu arg arg ser leu lys thr ile leu thr tyr ala glu glu asp met gly leu arg asp

422 452
AGC ACC TTC GCA GAG CAG GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG ATC CTG ACG GAC
ser thr phe ala glu gln val gln asp leu met phe asn leu his met ile leu thr asp

482 512
ACG GTG AAG ATG AAG GAA CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC CTC ATG TAC AGA
thr val lys met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg

542 572
ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG CAG AAC ATG GCC
il ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu gln asn met ala

602 |xxxxxxxxxxxxxxxxx transmembrane domain xxxxxxxxxxxxxx
GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG GTG CAC GCG GCC
gly lys his ala glu leu gly asn his ala glu ala ala gln cys met val his ala ala

XXXXXXXXXXXXXXXXXXXXXXXXXXXX|

692

GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAC CGC CAC CTG CCC GTG GGC TGC
ala leu val ala glu tyr leu ala leu l u glu asp his arg his leu pro val gly cys

722

752

GTT TCC TTC CAG AAC ATC TCA TCC AAT GTG CTA GAG GAG TCC GCC ATC TCC GAC GAC ATC
val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile ser asp asp ile

782

812

CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG CTG GGG CTG GTA
leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu leu gly leu val

842

872

GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC GAG GCG GTG AAT
gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr glu ala val asn

902

932

GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC AAG AAG CTG GCC
glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr lys lys leu ala

962

992

CCG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG AGT TCC GGC TGG
ala val his gly lys leu gln glu ala phe thr lys ile met his gln ser ser gly trp

1022

|xxxxx ITAM xxxxx|1052

GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC TTC GGT GAC CTG
glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his phe gly asp leu

1082

1112

GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA GAG ATC TCA CAC
asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala glu ile ser his

1142

1172

CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG ATT ATC AAA GAC
arg leu glu glu phe tyr thr glu arg phe gly asp asp val val glu ile ile lys asp

1202

1232

TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC CAG ATC ACG TAT
ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile gln ile thr tyr

1262

1292

GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC TTT GAC CGC AAC
val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr phe asp arg asn

1322

1352

TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG CGC GCA CAC GGG
tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly arg ala his gly

1382 1412
GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC GCC TTC CCC TAC
glu 1 u pro glu gln his lys arg lys thr leu leu ser thr asp his ala ph pro tyr

1442 1472 |xxxxxxxxxxx
ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG CCA GTG GAG GTG
ile lys thr arg ile arg val cys his arg glu glu thr val leu thr pro val glu val

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coile coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC GAG CAG GAC CCA
ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr glu gln asp pro

xx|
CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC ACC GTG AAC CAG
pro asp ala lys met leu gln met val leu gln gly ser val gly pro thr val asn gln

1622 1652
GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC CCC AAG CTC TTC
gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp pro lys leu phe

1682 1712
CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA TGT GAG GAT GCG
arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys cys glu asp ala

xx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC CGT GAG CTG GAG
leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his arg glu leu glu

xx|
CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG CGC CTG CCC CAG
arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln arg leu pro gln

1862 1892
CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA AGT TTC CGA AAG
leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala ser phe arg lys

1922 1952
GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG CAC CCG GGC CTC
ala asp leu STP

1982 2012
AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT GGG GTG ACC ACA

2042 2072
CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA CTG ATG CTT CCT

2102 2132
CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

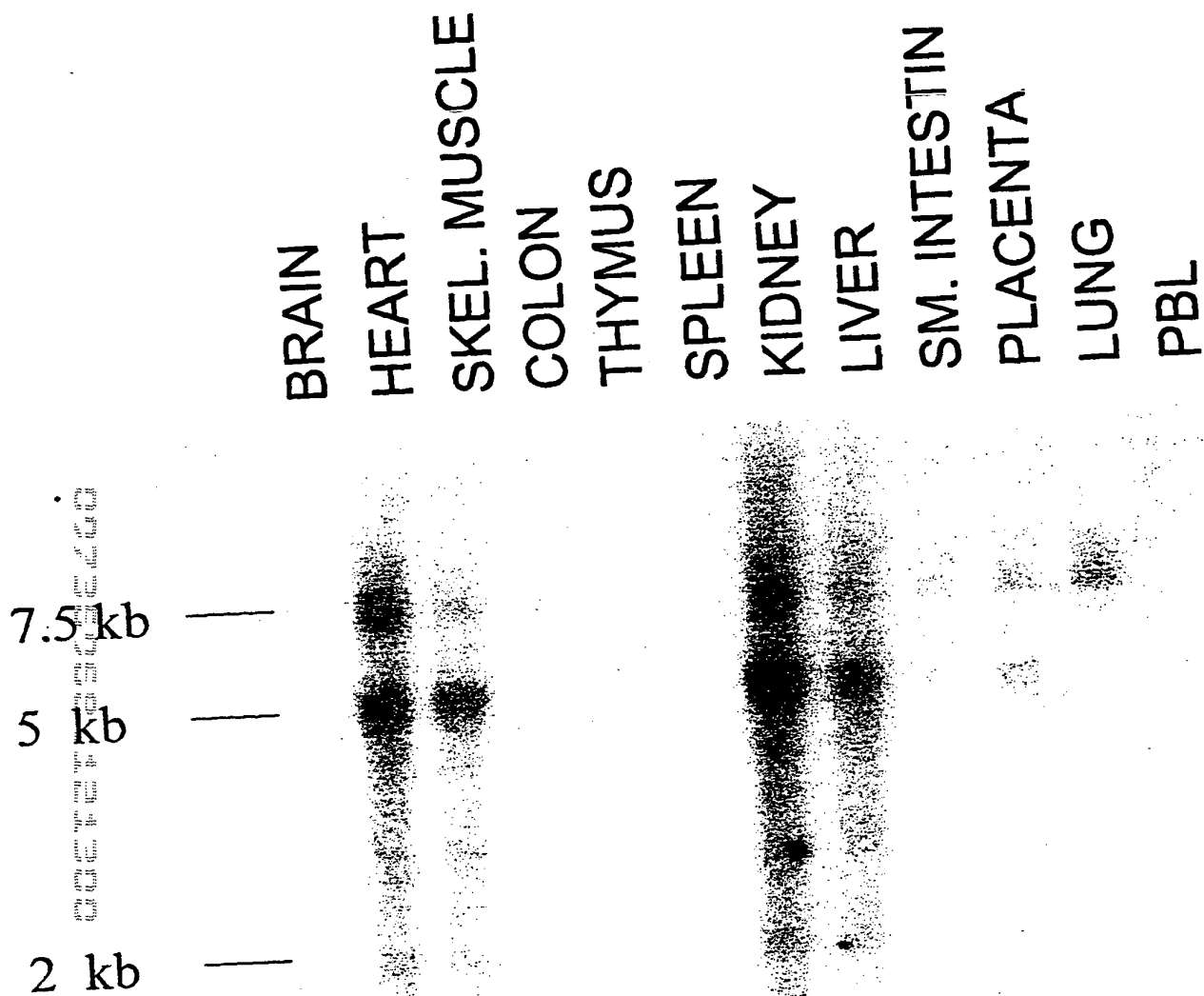


FIG. 2

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----VLHHHQNPEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVETRSAFAAVLHHHQNPEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDRVVTSEQHI
KIAA	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----

HC2A	OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPSPDDEVRSIIGSKGLDRSNSWNTGGPKAAPWGSNPSPSAES
HC5	-----

HC2A	IIHVVAQC	GLESHLRSYVKYAYKAEPYVASEYKTVHEE	KSMTTILKPSADFLTSN
KIAA	IIHVVAQC	HEEGLESHLRSYVKYAYKAEPYVASEYKTVHEEL	TKSMTTILKPSADFLTSN
rat			
HC4	LFHIVSKCHEEGLD	SYLSSFIKYSFRPGKPSAPOAPLIHETLATMMIAL	LKQSADFLAIN
HC1	LPDIVAKCHEEQ	LDHSVQSYIKFVFKTR---	ACKERPVEDLAKNVTGLLK-SNDSPTVK
HC3	TQAMDRSCNRMSSHT	TETSSFLQTLTGRLP---	TKKLFHEELALQWVVCSG--SVR---E
HC5			

Cadherin
Cleavage

HC2A	KLLRYSWFFFDVLI	KSMQHLIENSKVKLIRNQRFPASYHHA	AETVVMMLMPHITQKFGD
KIAA	KLLKYSWFFFDVLI	KSMQHLIENSKVKLIRNQRFPASYHHA	VETVVMMLMPHITQKFRD
rat			
HC4	KLLKYSWFFFEI	IAKSMATYLLLEENKIKLTHGQRF	PKAYHHAHLSLFLAIT-IVESQYAE
HC1	HVLKHSWFFFAI	ILKSMQHLIDTNKIQLERPQRF	PESYQNELDNLMVLSDHVIWKYKD
HC3	SALQQAWFFFE	LMVKSVMVHLYFNDKLEAPRKS	RFPERFMDIAALVSTIASDIVSRFQK
HC5			

HC2A	NPEASKNANHSLAV	FIKRCFTFMDRGFVFKQIN---	NYIS--CFAPGDPKTLFEYKFEFL
KIAA	NPEASKNANHSLAV	FIKRCFTFMDRGFVFKQIN---	NYIS--CFAPGDPKTLFEYKFEFL
rat			
HC4	IPKESRNVNYS	SLASFLKCCLTLMDRGFVFNLIN---	DYIS--GFSPKDPKVLAEYKFEFL
HC1	ALEETRRATHS	VARFLKRCFTFMDRGCVFKMVN---	NYIS--MFSSGDLKTLQYKFDL
HC3	DTEMVERLNTS	LAFFLNDLLSVMDRGFVFSLIK	SCYQVSSKLYSLPNPSVLVSLRLDFL
HC5			

HC2A	RVVCNHEHYIPLNLPM----	PFGKGRIQR-----	YQDLQL----	DYSLTDEF
KIAA	RVVCNHEHYIPLNLPM----	PFGKGRIQR-----	YQDLQL----	DYSLTDEF
rat				
HC4	QTICNHEHYIPLNLPM----	AFAPKPLQR-----	VQDSNL----	EYSLSDEY
HC1	QEVCOHEHFIP	LCPLIRSANIPDPLTPSES-----	TQELHASDMPEYSVTNEF	
HC3	RIICSHEHYVT	LNLPSCSLTPPASPSVSSATSQSSGFSTNVQDQKIANMFELS--	VPF	
HC5				

Cadherin
EC motif

HC2A	CRNHFLVGILLRE	VGTA	LQEFRE----	VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA	CRNHFLVGILLRE	VGTA	LQEFRE----	VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat				
HC4	CKHHFLVGILLRE	TSIALQDNYE----	IRYTAISVIKNLLIKHAFDTRYQHKNQQA	KIAQ
HC1	CRKHFLIGILLRE	VGFA	LQEDQD----	VRHLALAVLKNLMAKHSFDDRYREPRKQAOIAS
HC3	RQOHYLAGIVL	TELAVILDPDAEGLFGLHKKVINMVHNLSSHDS	DPYSDPQIKARVAM	
HC5	SSTS-SPGL	FTLAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPR	CVKPEVKV	KIAA

HC2A	LYLPLFGLLIEN	VQRINVRDVSPFPVNAG-MTVKDES	LALPAVNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLIEN	VQRINVRDVSPFPVNAG-MTVKDES	LALPAVNPLVTPQKGSTLDNSLH
rat			
HC4	LYLPFVGILL	ENIQRLAGRTLYSCAMPNSASRDEFPCG----	FTSP--AN--RGSLS
HC1	LYMPLYGMLLD	NMPRIYKDLYPFTVNTSNQGSRDDLS	TNGGFQSQTAIKHANSVDTSFS
HC3	LYLPLIGI	IMETVPQLYDFTETHNQGRPIC	IATDDYESE-----SG--SMIS
HC5	LYLPLVGI	ILDALPQLCDFTVADTRRYR---	TSGSDEEQE-----GA---GAIT

HC2A	KDLLGAISG	●	PYTTSTPNINSVRNADSRGSLISTDSGNS	●	RNSEKSNSLDKHQSS
KIAA	KDLLGAISG	●	PYTTSTPNINSVRNADSRGSLISTDSGNS	●	RNSEKSNSLDKHQSS
rat	-----				
HC4	TDKDTAYGSFQNG	-----	HGIKREDSRGS	LIP-EGATGFPDQGN	TGEN-----TRQS
HC1	KDVLNSIAAFSS	-----	IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL		
HC3	QTVAMAIAGTSVPQ	-----	LTRPGSFLLTSTSGRQHT	-----	
HC5	QNVALAIAGNNFN	-----	LKTSG-IVLSSLPYKQYN	-----	
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTI	SEVCL			
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTI	SEVCL			
rat	-----				
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISED	TLLTYWN-KVSPQELINILILLEVCL			
HC1	ALIGSTLRFDRLDQAE	TRSLLMCFHIMKTI SYETLIAYWQ-RAPSPEVSDFFSILDVCL			
HC3	-----T	FSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLDLLLYLCV			
HC5	-----M	LNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV			
HC2A	HQFOYMGKRYIARNQ	EGLG--PIVHDRKS		-----QTLPVSRNRTGMM	
KIAA	HQFOYMGKRYIAR	-----		-----TGM	
rat	-----				
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS	-----QTMPALNRNSGVM			
HC1	QNFRLGKRNIIRKIAAF	--KFVQSTQNNGLKGSNPSCQTSGLLAQWMHSTSRHEGHK			
HC3	SCFEYKGGKVFERN	SLTFK--KSKDMRAK		-----LEEAILGSIGARQEMV	
HC5	LCFEYKGGQSSDKVSTQVLQ	--KSRDVKAR		-----LEEALLRGE	
HC2A	HARLQQL	-----GSLDNS		-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
KIAA	HARLQQL	-----GSLDNS		-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
rat	-----				
HC4	QARLQHL	-----SSLESS		-----FTLNHSSTTTEADI FHQALLEGNTATEVS	
HC1	QHR	SOTLPIIRGK--NALS		NPKL----LQMLDNTMTS	
HC3	RRSRGQLERS	PSGSAFGSQENLRWRKDMTHWRQNT		EKLDKSRAEIEHEALIDGNLATEAN	
HC5	RRRAPGNDRFP	----GLNENLRWKKEQTHWRQANEKLDKTKAELDQ		EALISGNLATEAH	
HC2A	LTALDTLSLFTLAFKNQLLADHGHNP	LMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY			
KIAA	LTALDTLSLFTLAFKNQLLADHGHNP	LMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY			
rat	-----KLSRGHSP				
HC4	LTVLDTISFFTQCFKTHFLNNDGHNP	LMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS			
HC1	LTILDVLSLFTQTHQRLQ	QCDCQNSLMKRGFDTYMLFFQVQNQSATALKHVFASLRLFC			
HC3	LIILD	TLEIVVQTVS--VTES--KESILGGVLKVLHSMACNQSAVYLQHC		FATORALVS	
HC5	LIILD	MQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNC		DQSTTYLTHCFATLRALIA	
HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRN	NFDYTGKKSFVRTH			
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRN	NFDYTGKKSFVRTH			
rat	KFPSTFYEGRADMCAALCYEVLKCCNSKLSSIRTEASQLLYFLMRN				
HC4	KFP	SAFFKGRVNMCAAF		CYEVLKCCTSKISSRNEASALLYLLMRNFEYTKRKTFLRTH	
HC1	KFPS	AFFQGPADLCGSFCYEVLKCCNHR		SRSTQTEASALLYLFMRKNFEFNKQKSIVRSH	
HC3	KFPELLFEEETE	QCADLCRLRLRH		CSSSIGTIRSHPSASLYLLMRQNF	
HC5	KFGDLLFEEVE	QCFDLCHQVLHHCSSSMDVTRS		QACATLYLLMRFSFGATS--NFARVK	
HC2A	LQVIIISVSQLIADVVGIGETR	FQQSLSIINN			
KIAA	LQVIIISVSQLIADVVGIGETR	FQQSLSIINN			
rat	CANS				
HC4	LQII	IIVS		QLIADVALSGGSRFQESLFIINN	
HC1	LQLIKAVS	QLIAD-AGIGGSR		FQHS	
HC3	MQVPMS	LSSLVGTSQNFEEFLRRSLK		TILTYAEEDLELRETTFPDQVQDLVFNLMHILS	
HC5	MQVTMS	LASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQ		MTPPPTQVEELL	

FIG. 3
3 of 5

	Transmembrane
HC2A	ATAQMK EHENDPEMLVDLQYSLAKSYASTPELRK TWLDSMARIHVKNGLSEAAAMCYVHV
KIAA	ATAQMK EHENDPEMLVDLQYSLAKSYASTPELRK TWLDSMARIHVKNGLSEAAAMCYVHV
rat	ATAQMK EHENDPEMLVDLQYSLAKSYASTPELRK TWLDSMARIHVKNGLSEAAAMCYVHV
HC4	ATAQMK EHKDP PEMLIDLQYSLAKSYASTPELRK TWLDSMA IKHVKNGLFSEAAAMCYVHV
HC1	ATAQMK EHKDP PEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGILSEAAAMCYIHI
HC3	DTV KMK EHQEDPEMLIDLMYRIAKGYQTS PD LRLTWLQNMAGKHSERSNHAEEAAQCLVHS
HC5	DTV KM REFQEDPEMLMDLMYRIAKSYQAS PD LRLTWLQNMAEKHTKKKCYTEAAMCLVHA

	domain	SH3	
HC2A	TALVAEYILTRKGV-----		FRQGCTAFRVITPN
KIAA	TALVAEYILTRKEA-----	VQWEPPLLP PHSHSACLR SRGGVFRQGCTAFRVITPN	
rat	TALVAEYILTRKEAD-----	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN	
HC4	AALVAEFLHRKKL-----		FPNGCSAFKKITPN
HC1	AALIAEYILKRKG YWKVEKIC	TASLLSE DP THPCDSNSLLTTPSGGSMFSMGWPAFLSITPN	
HC3	AALVAEYILSMLED-----		RKYLPGVCVTFQNISSN
HC5	AALVAEYILSMLED-----		HSYLPVGSVSFQNISSN

	ITAM
HC2A	IDEEASMMEDVGMQD-----VHF NEDVLMELLEQC ADGLWKAERYELIADIYKLIPIPI
KIAA	IDEEASMMEDVGMQD-----VHF NEDVLMELLEQC ADGLWKAERYELIADIYKLIPIPI
rat	IDEEASMMEDVGMQD-----VHF NEDVLMELLEQC ADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD-----VHYSEEVLLELLEQCVNGLWKAERYEITSEISKLI GPI
HC1	IKEEGAAKEDSGMHD-----TPYNENILVEQLYMCGEFLWKSEYELIADV NKPI IAV
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVLIP I
HC5	VLEESV V SED T LS P DE D GVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIP I

	ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD-----			
KIAA	YEKRRD FERLAHL YDTI HRAY SKVTEVMHSGRRLLGTYFRVAF FGQAAQYQFTD SETDVE			
rat	SMKSGGTLE THLY DTI HR PYSKVTEVITR-----A-----AGSWDLLPGGLFGQ			
HC4	YENRREFENLTQVYRTIHGAYTKILEVMHTKKRLG-----TFFRVAFY GQ			
HC1	FEKQ RDF KKLS DL YD I HRSYLKVAEVVNSEKRLFG-----FYRVAFY GQ			
HC3	HEANRDAKKLSTIHGKLQEA FSKIV HQSTGWERMFG-----TYFRVGFY G			
HC5	LEAHREFRKLTLTHSKLQRA FDSIV NKDH--KRMFG-----TYFRVGF FFG			

	ITAM	ITAM
HC2A	-FFEDEDGKE YIYKE PKLTPLSEISQRL LLK YSDRFGSENVKMIQDSGKVNPKDLDSKYA	
KIAA	GFFEDEDGKE YIYKE PKLTPLSEISQRL LLK YSDRFGSENVKMIQDSGKVNPKDLDSKYA	
rat	GFFEDEDGKE YIYKE PKLTPLSEISQRL LLK YSDRFGSENVKMIQDSGKVNPKDLDSKYFA	
HC4	SFFEEDGKE YIYKE PKLTGLSEISLRLV KI YGERFGTENVKIIQSDSKVNAKELDPKYA	
HC1	GFFEEEEGKE YIYKE PKLTGLSEISQRL LLK YADRF GAD NVKIIQDSNKNVNPKDLDPKYA	
HC3	TKFGDLDEQEFVYKEPAITKLA EIS HRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA	
HC5	SKFGDLDEQEFVYKEPAITKLP EIS HRLEAFY GQC FGAEFVEVIK D STPVDKTKLDPNKA	

	ITAM
HC2A	YI Q VTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGV EEQ CKRRTILTA
KIAA	YI Q VTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGV EEQ CKRRTILTA
rat	YI Q VTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGV EEQ CKRRTILTA
HC4	HI Q VTVYKPYFDDKELTERKTEFERHNISRFVFEAPYTL SGKKQ GCI EEQ CKRRTILTT
HC1	YI Q VTVYVTPFFEEKEIEDRKTD FEM HHNINRFVFETPFTLSGKKHGGV AEQ CKRRTILTT
HC3	YI Q ITYVEPYFD TYEM KDRITYFDKNYNLRRFMYCTPFTLDGRAH GEL HEQFKRRTILTT
HC5	YI Q ITFVEPYFDEYEMKDRV TYFE KNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTT

Coiled-Coil 1

HC2A	IHC	FPYVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELRQLC	SSAEVDMIKLQLKLQGSV
KIAA	IHC	FPYVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELRQLC	SSAEVDMIKLQLKLQGSV
rat	IHC	FPYVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELHQLC	SSAEVDMIKLQLKLQGSV
HC4	SNS	FPYVKKRIPIN	CEQQINLKE	IDGATDEIKDKTAELOKLC	SSTDVDMIQLQLKLQGSV
HC1	SHL	FPYVKKRIQV	ISQSSTELN	IEVAIDEMSRKVSELNQLCT	MEEVDMISLQLKLQGSV
HC3	SHAF	PIKTRVNVTH	KEEIILTR	IEVAIEDMQKKTQELAFATH	QDPADPKMLQMLVQGSV
HC5	MHAF	PIKTRISVIQ	KEEFVLTR	IEVAIEDMKKKTLLQAVAIN	QEPDAKMLQMLVQGSV

Coiled-Coil 2

HC2A	SVQVNAGPLAYARAFLDDTNTKRYPD	KNVKLLKEVFRQFVEACGQ	FLAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLDDTNTKRYPD	KNVKLLKEVFRQFVEACGQ	FLAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLDDTNTKRYPD	KNVKLLKEVFRQFVEACGQ	FLAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLNDSQASKYPP	KKVSELKDMFRKFIQACSIA	LELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLEETNAKKYP	DNQVKLLKEIFRQFADACGQ	ALDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKL	FRHHNKLRLCFKDFTKRCED	ALRKNSLIGPVQKE
HC5	GATVNQGPLEVAQVFLAEIPADPKL	YRHHNKLRLCFKEFIMRCGEA	VEKNKRLITADQRE

Coiled-Coil 2

HC2A	YQEEMKANYREMAKELSEIMHE	QICPLEEKTS-VLPNSLHIFNAISG	TPTSTMVHGMTSS
KIAA	YQEEMKANYREMAKELSEIMHE	QLG-----	
rat	YQEEMKANYREIRKELSDIIVER	ICPGEDKRATKFP	PAHLQRHQ
HC4	YHEGLKSNFRDMVKELSDIHE	QILOEDTMHSPWMSNTLHV	FCAISGTSSDRGYGSPRYA
HC1	YQEELRSHYKDMSELSTVMNE	QITGRDDLK---	RGVDQTCTRVISKATPALPTVSISS
HC3	YQRELG----	KLSS-----	PZ-----
HC5	YQOELKKNYNKLKENLRPMIER	KIPELYKPIFRVESQKRDS	FHRSSFRCETQLSQGSZ-

PBM

HC2A	SSVVZ-----
KIAA	-----
rat	-----
HC4	CVTLPHPEPHVGTCTFVMCKLR
HC1	TTFRANHWFCQAQEEAMNGREKE
HC3	PWTVIFNSRFYRSWGK
HC5	EVZ-----
	SAEVZ-----

HC2A	----
KIAA	----
rat	VHIF
HC4	----
HC1	----
HC3	----
HC5	----

C

D

B

F

G

CLASP-1	SEQLKLOGSVSVKVNAG	PMAYARAFLEETNAKKY	PNQV--KLLKEIFRQFADACGQALD
TRG	KLQKLOGSVSVQVNAG	PLAYARAFLLDDTNTKRY	PNKV--KLLKEVFROFVEACGOALA
KIAA1056	KLQKLOGSVSVQVNAG	PLAYARAFLLDDTNTKRY	PNKV--KLLKEVFROFVEACGOALA
CLASP-2	KLQKLOGSVSVQVNAG	PLAYARAFLLDDTNTKRY	PNKV--KLLKEVFROFVEACGOALA
CLASP-6	KLQKLOGSVSVQVNAG	PLAYARAFLLDDTNTKRY	PNKV--KLLKEVFROFVEACGOALA
CLASP-3	MLQMVLOGSVGTTVNQG	LEVAQVFLSE--IPSDPKLFRHHNKLRLCFKDFTKRCEDALR	
CLASP-4	QLQKLOGCVSVQVNAG	PLAYARAFLLDSQASKYPPKKVSELKDMFRKFI--QACSI	ALE
CLASP-5	MLQMVLOGSVGATVNQG	LEVAQVFLAE--IPADPKLYRHHNKLRLCFKEFIMRCGEAVE	
KIAA0716	PLTMCLNGVIDAAVNGGV	SRYQEAFFVKEYILSHPE	EDGEKIARLRELMLEQAQILEFGLA
DOCK2	PLSMLLNGIVDPAVMGG	FAKYEKAFFTEEYVRDHP	EDQDKLTHLKDLIAWQIPFLGAGIK
DOCK3	LLSMCLNGVIDAAVNGGI	ARYQEAFFDKOYINKHP	GDAEKITQLKELMQEQVHVLGVGLA
DOCK180	PLSMLLNGIVDPAVMGG	FAKYEKAFFTEEYVRDHP	EAHEKIEKLKDLIAWQIPFLAEGIR
CONSENSUS	L M L+G V VN G	Y AFL + + P	L+
	L I	V V F +	I

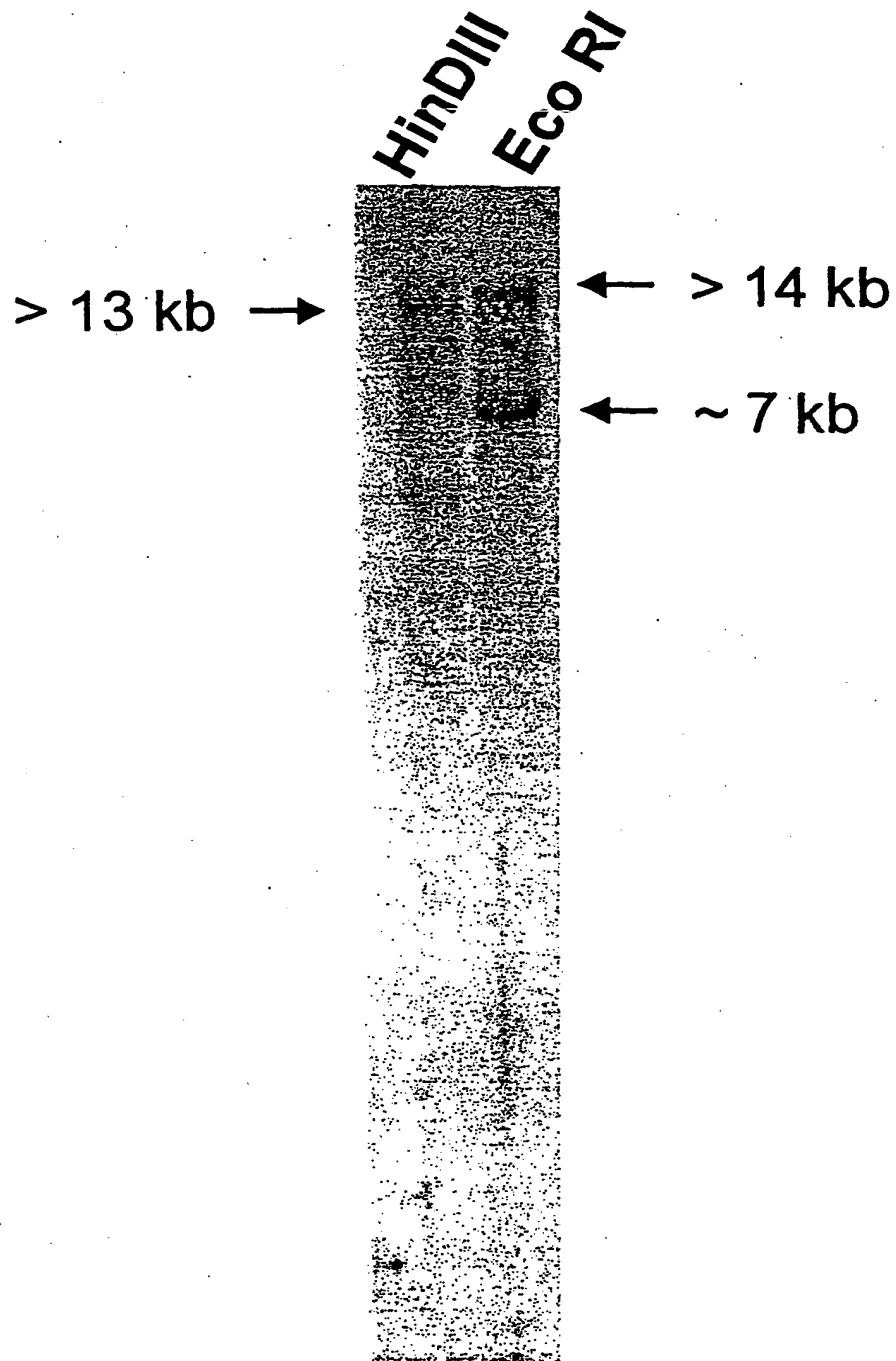
DOCK1=KIAA0209

DOCK3=KIAA0299

CLASPvariant=KIAA1055

B

FIG. 3
2 of 2



genomic DNA

FIG. 4

-12 -1
GACGCGAGGACC

1/1	31/11
ATG GCT GCC TCC GAG CGC CGC GCC TTC GCG	CAC AAG ATC AAC AGG ACG GTG GCC GCA GAG
Met ala ala ser glu arg arg ala phe ala	his lys ile asn arg thr val ala ala glu
61/21	91/31
GTG CGG AAG CAG GTG TCC CGG GAA CGC AGT	GGC TCC CCC CAC TCC AGC AGG CGC TGC AGC
val arg lys gln val ser arg glu arg ser	gly ser pro his ser ser arg arg cys ser
121/41	151/51
AGC TCC CTG GGG GTC CCA CTG ACT GAA GTT	GTC GAG CCC CTG GAC TTT GAG GAT GTA CTT
ser ser leu gly val pro leu thr glu val	val glu pro leu asp phe glu asp val leu
181/61	211/71
CTG AGC CGG CCA CCA GAT GCT GAG CCC GGG	CCC CTC AGG GAC CTG GTA GAA TTC CCA GCT
leu ser arg pro pro asp ala glu pro gly	pro leu arg asp leu val glu phe pro ala
241/81	271/91
GAT GAC TTG GAG CTG CTG CTG CAG CCC CGG	GAA TGC CGG ACC ACG GAG CCC GGG ATC CCC
asp asp leu glu leu leu leu gln pro arg	glu cys arg thr thr glu pro gly ile pro
301/101	331/111
AAG GAT GAA AAA CTG GAT GCC CAG GTG AGG	GCC GCG GTG GAG ATG TAT ATT GAG GAC TGG
lys asp glu lys leu asp ala gln val arg	ala ala val glu met tyr ile glu asp trp
361/121	391/131
GTC ATT GTC CAC AGA AGG TAT CAG TAC CTG	AGT GCA GCA TAC AGC CCC GTC ACC ACA GAC
val ile val his arg arg tyr gln tyr leu	ser ala ala tyr ser pro val thr thr asp
421/141	451/151
ACA CAG CGG GAG CGA CAG AAG GGC CTC CCC	CGC CAG GTC TTT GAG CAG GAT GCT TCT GGA
thr gln arg glu arg gln lys gly leu pro	arg gln val phe glu gln asp ala ser gly
481/161	511/171
GAC GAG AGG TCC GGC CCT GAG GAC TCG AAT	GAC TCC CGG CGT GGC TCG GGC TCC CCG GAA
asp glu arg ser gly pro glu asp ser asn	asp ser arg arg gly ser gly ser pro glu
541/181	571/191
GAC ACC CCT CGA AGC AGT GGT GCC TCT AGC	ATC TTC GAC CTG AGG AAC CTG GCA GCT GAC
asp thr pro arg ser ser gly ala ser ser	ile phe asp leu arg asn leu ala ala asp
601/201	631/211
TCA TTG CTG CCC TCT CTG CTA GAG CGG GCG	GCC CCA GAA GAT GTG GAC CGG CGC AAT GAA
ser leu leu pro ser leu leu glu arg ala	ala pro glu asp val asp arg arg asn glu
661/221	691/231
ACC CTT CGA CGG CAG CAC CGG CCC CCG GCC	CTG CTC ACC CTC TAC CCG GCA CCT GAC GAG
thr leu arg arg gln his arg pro pro ala	leu leu thr leu tyr pro ala pro asp glu
721/241	751/251
GAT GAA GCC GTG GAA CGC TGT AGC CGC CCA	GAG CCA CCC CGC GAG CAC TTT GGA CAA AGG
asp glu ala val glu arg cys ser arg pro	glu pro pro arg glu his phe gly gln arg
781/261	811/271
ATC TTG GTC AAG TGT CTG TCG CTC AAG TTC	GAG ATT GAA ATT GAG CCC ATC TTT GGG ATC
ile leu val lys cys leu ser leu lys phe	glu ile glu ile glu pro ile phe gly ile
841/281	871/291
TTG GCT CTG TAT GAT GTG CGG GAG AAA AAG	AAG ATC TCG GAG AAC TTC TAC TTC GAC CTG
leu ala leu tyr asp val arg glu lys lys	lys ile ser glu asn phe tyr phe asp leu
901/301	931/311
AAC TCG GAC TCC ATG AAG GGG CTG CTT CGG	GCT CAT GGC ACC CAC CCT GCC ATC TCC ACC
asn ser asp ser met lys gly leu leu arg	ala his gly thr his pro ala ile ser thr
961/321	991/331
CTG GCC CGC TCT GCC ATC TTC TCT GTG ACC	TAC CCC TCA CCT GAC ATC TTC CTG GTC ATC
leu ala arg ser ala ile phe ser val thr	tyr pro ser pro asp ile phe leu val ile
1021/341	1051/351
AAG TTG GAG AAG GTG CTT CAG CAA GGG GAC	ATC AGT GAG TGC TGT GAG CCT TAC ATG GTG
lys leu glu lys val leu gln gln gly asp	ile ser glu cys cys glu pro tyr met val
1081/361	1111/371

TTG AAA GAA GTG GAC ACA GCC AAG AAC AAA GAG AAG CTA GAG AAG CTG CGC CTG GCG GCC
 leu lys glu val asp thr ala lys asn lys glu lys leu glu lys leu arg leu ala ala
 1141/381 1171/391
 GAG CAG TTC TGC ACC CGC CTG GGC CGC TAC CGC ATG CCC TTC GCC TGG ACG GCC GTG CAC
 glu gln phe cys thr arg leu gly arg tyr arg met pro phe ala trp thr ala val his
 1201/401 1231/411
 TTG GCC AAC ATC GTG AGC AGC GCT GGG CAG CTG GAC CGG GAC TCT GAC TCG GAG GGC GAG
 leu ala asn ile val ser ser ala gly gln leu asp arg asp ser asp ser glu gly glu
 1261/421 1291/431
 CGC CGG CCA GCC TGG ACA GAC CGC CGC CGT CGG GGG CCC CAG GAC CGG GCG AGT AGT GGG
 arg arg pro ala trp thr asp arg arg arg arg gly pro gln asp arg ala ser ser gly
 1321/441 1351/451
 GAC GAC GCC TGC AGC TTC TCT GGC TTC CGT CCA GCC ACG CTA ACT GTC ACA AAC TTC TTT
 asp asp ala cys ser phe ser gly phe arg pro ala thr leu thr val thr asn phe phe
 1381/461 1411/471
 AAG CAG GAG GCT GAG CGA CTC AGT GAC GAG GAC CTC TTC AAG TTC CTG GCT GAC ATG AGG
 lys gln glu ala glu arg leu ser asp glu asp leu phe lys phe leu ala asp met arg
 1441/481 1471/491
 CGC CCG TCG TCC CTG CTG CGG CGA CTA CGT CCT GTG ACT GCC CAG CTC AAG ATC GAC ATT
 arg pro ser ser leu leu arg arg leu arg pro val thr ala gln leu lys ile asp ile
 1501/501 1531/511
 TCT CCG GCT CCT GAA AAT CCC CAC TTC TGC CTC TCC CCT GAG CTG CTT CAT ATC AAG CCC
 ser pro ala pro glu asn pro his phe cys leu ser pro glu leu leu his ile lys pro
 1561/521 1591/531
 TAC CCG GAC CCC AGG GGC CGG CCC ACC AAG GAG ATT CTG GAG TTC CCC GCC CGC GAA GTC
 tyr pro asp pro arg gly arg pro thr lys glu ile leu glu phe pro ala arg glu val
 1621/541 1651/551
 TAT GCC CCC CAT ACC AGC TAC AGG AAC CTG CTG TAC GTG TAC CCG CAC AGC CTC AAC TTC
 tyr ala pro his thr ser tyr arg asn leu leu tyr val tyr pro his ser leu asn phe
 1681/561 1711/571
 AGC AGC CGC CAG GGC TCC GTG CGC AAC CTT GCT GTG CGA GTG CAG TAC ATG ACA GGC GAG
 ser ser arg gln gly ser val arg asn leu ala val arg val gln tyr met thr gly glu
 1741/581 1771/591
 GAC CCC AGC CAG GCT CTG CCG GTC ATC TTT GGC AAG TCC AGC TGC AGT GAA TTT ACC CGC
 asp pro ser gln ala leu pro val ile phe gly lys ser ser cys ser glu phe thr arg
 1801/601 1831/611
 GAG GCC TTC ACA CCG GTG GTC TAC CAT AAC AAG TCC CCC GAG TTC TAC GAG GAG TTC AAG
 glu ala phe thr pro val val tyr his asn lys ser pro glu phe tyr glu glu phe lys
 1861/621 1891/631
 CTG CAT CTT CCA GCC TGC GTG ACA GAG AAC CAT CAC CTG CTG TTC ACC TTC TAC CAT GTC
 leu his leu pro ala cys val thr glu asn his his leu leu phe thr phe tyr his val
 1921/641 1951/651
 AGC TGC CAG CCC CGG CCG GGC ACT GCC CTG GAG ACA CCC GTG GGC TTT ACT TGG ATC CCA
 ser cys gln pro arg pro gly thr ala leu glu thr pro val gly phe thr trp ile pro
 1981/661 2011/671
 CTG CTG CAG CAC GGG CGC CTG AGG ACC GGC CCC TTC TGT CTC CCA GTG TCT GTG GAC CAG
 leu leu gln his gly arg leu arg thr gly pro phe cys leu pro val ser val asp gln
 2041/681 2071/691
 CCG CCG CCC AGC TAT TCC GTG CTC ACA CCC GAT GTG GCG CTT CCG GGC ATG CGC TGG GTG
 pro pro pro ser tyr ser val leu thr pro asp val ala leu pro gly met arg trp val
 2101/701 2131/711
 GAC GGT CAC AAG GGC GTG TTC AGT GTG GAG CTC ACA GCC GTG TCC TCT GTG CAC CCC CAG
 asp gly his lys gly val phe ser val glu leu thr ala val ser ser val his pro gln
 2161/721 2191/731
 GAC CCC TAC CTG GAC AAA TTC TTC ACC CTG GTG CAC GTC CTG GAG GAG GGA GCC TTC CCA
 asp pro tyr leu asp lys phe phe thr leu val his val leu glu glu gly ala phe pro
 2221/741 2251/751
 TTC CGG CTC AAG GAC ACT GTG CTG AGC GAG GGC AAC GTG GAG CAG GAG CTG CGG GCC AGT
 phe arg leu lys asp thr val leu ser glu gly asn val glu gln glu leu arg ala ser
 2281/761 2311/771
 CTT GCA GCA CTG CGC CTG GCC AGC CCC GAA CCC CTT GTG GCC TTC TCC CAC CAC GTG CTG

leu ala ala leu arg leu ala ser pro glu pro leu val ala phe ser his his val leu
 2341/781 2371/791
 GAC AAG CTC GTG CGT CTG GTC ATC AGG CCC CCG ATC ATC AGT GGC CAG ATT GTG AAC CTG
 asp lys leu val arg leu val ile arg pro pro ile ile ser gly gln ile val asn leu
 2401/801 2431/811
 GGC CGT GGA GCC TTT GAA GCA ATG GCC CAT GTA GTC AGC CTT GTT CAC CGG AGC CTG GAG
 gly arg gly ala phe glu ala met ala his val val ser leu val his arg ser leu glu
 2461/821 2491/831
 GCA GCC CAG GAT GCC CGC GGT CAC TGC CCA CAG CTG GCT GCC TAC GTC CAC TAC GCC TTT
 ala ala gln asp ala arg gly his cys pro gln leu ala ala tyr val his tyr ala phe
 2521/841 2551/851
 CGC CTT CCT GGC ACT GAG CCC AGC CTC CCG GAT GGG GCC CCT CCA GTG ACA GTG CAG GCT
 arg leu pro gly thr glu pro ser leu pro asp gly ala pro pro val thr val gln ala
 2581/861 2611/871
 GCC ACA CTG GCC CGT GGC TCT GGT CGC CCC GCA AGC CTC TAC CTG GCG CGT TCC AAG AGC
 ala thr leu ala arg gly ser gly arg pro ala ser leu tyr leu ala arg ser lys ser
 2641/881 2671/891
 ATC AGC AGC AGC AAC CCT GAC CTC GCC GTG GCC CCT GGC TCT GTG GAT GAC GAG GTT TCC
 ile ser ser ser asn pro asp leu ala val ala pro gly ser val asp asp glu val ser
 2701/901 2731/911
 CGC ATC CTG GCC AGC AAG CTG CTT CAC GAG GAG CTG GCT CTG CAG TGG GTG GTC AGC AGC
 arg ile leu ala ser lys leu leu his glu glu leu ala leu gln trp val val ser ser
 2761/921 2791/931
 AGT GCC GTA CGC GAG GCC ATC CTC CAG CAC GCC TGG TTC TTC TTC CAG CTC ATG GTG AAG
 ser ala val arg glu ala ile leu gln his ala trp phe phe phe gln leu met val lys
 2821/941 2851/951
 AGT ATG GCG CTG CAC CTG CTG CTT GGC CAG CGA CTA GAC ACA CCC CGC AAG CTG CGC TTC
 ser met ala leu his leu leu leu gly gln arg leu asp thr pro arg lys leu arg phe
 2881/961 2911/971
 CCC GGA CGC TTC CTG GAC GAC ATC ACT GCC TTG GTG GGC TCT GTG GGC CTG GAG GTC ATC
 pro gly arg phe leu asp asp ile thr ala leu val gly ser val gly leu glu val ile
 2941/981 2971/991
 ACC CGT GTC CAC AAG GAT GTG GAG CTG GCC GAG CAC CTC AAC GCC AGC CTG GCT TTC TTC
 thr arg val his lys asp val glu leu ala glu his leu asn ala ser leu ala phe phe
 3001/1001 3031/1011
 CTC AGT GAC CTT CTG TCC CTG GTG GAC CGG GGC TTT GTC TTC AGC CTG GTC CGG GCC CAC
 leu ser asp leu leu ser leu val asp arg gly phe val phe ser leu val arg ala his
 3061/1021 3091/1031
 TAC AAG CAG GTG GCC ACG CGG CTC CAG TCG TCC CCT AAT CCA GCA GCC CTG CTG ACC CTG
 tyr lys gln val ala thr arg leu gln ser ser pro asn pro ala ala leu leu thr leu
 3121/1041 3151/1051
 CGC ATG GAA TTC ACC CGC ATC CTG TGC AGC CAC GAG CAC TAC GTG ACC CTC AAC CTC CCC
 arg met glu phe thr arg ile leu cys ser his glu his tyr val thr leu asn leu pro
 3181/1061 3211/1071
 TGC TGC CCC CTG TCA CCT CCA GCC TCG CCC TCC CCC TCT GTG TCC TCC ACC ACC TCC CAG
 cys cys pro leu ser pro pro ala ser pro ser pro ser val ser ser thr thr ser gln
 3241/1081 3271/1091
 AGC TCC ACC TTC TCC AGC CAA GCC CCG GAC CCC AAG GTG ACC AGC ATG TTC GAA CTG AGT
 ser ser thr phe ser ser gln ala pro asp pro lys val thr ser met phe glu leu ser
 3301/1101 3331/1111
 GGA CCA TTC CGG CAG CAG CAC TTC CTA GCT GGG CTC CTG CTG ACG GAG CTG GCA CTG GCC
 gly pro phe arg gln gln his phe leu ala gly leu leu leu thr glu leu ala leu ala
 3361/1121 3391/1131
 CTC GAA CCT GAG GCT GAA GGG GCA TTC CTG TTG CAC AAG AAG GCC ATC AGT GCT GTG CAC
 leu glu pro glu ala glu gly ala phe leu leu his lys lys ala ile ser ala val his
 3421/1141 3451/1151
 AGC CTG CTA TGT GGC CAT GAC ACT GAC CCC CGC TAC GCC GAG GCC ACT GTG AAG GCT CGT
 ser leu leu cys gly his asp thr asp pro arg tyr ala glu ala thr val lys ala arg
 3481/1161 3511/1171
 GTG GCC GAG CTG TAC CTG CCA CTG CTT TCG ATT GCA CGG GAT ACC TTG CCA CGG CTG CAT
 val ala glu leu tyr leu pro leu leu ser ile ala arg asp thr leu pro arg leu his

3541/1181	GAC TTT GCT GAG GGC CCA GGT CAG CGG TCA	3571/1191	AGA CTG GCC TCA ATG CTT GAC TCA GAC ACA
asp phe ala glu gly pro gly gln arg ser		arg leu ala ser met leu asp ser asp thr	
3601/1201	GAA GGC GAA GGG GAC ATT GCG GGT ACC ATC	3631/1211	AAC CCC TCT GTG GCC ATG GCC ATT GCT GGT
glu gly glu gly asp ile ala gly thr ile		asn pro ser val ala met ala ile ala gly	
3661/1221	GGC CCC CTA GCC CCT GGC TCC CGG GCC AGC	3691/1231	ATC TCC CAG GGG CCA CCA ACG GCT TCT CGC
gly pro leu ala pro gly ser arg ala ser		ile ser gln gly pro pro thr ala ser arg	
3721/1241	GCA GGC TGT GCC CTC TCT GCT GAG TCA AGC	3751/1251	CGG ACC TTG CTG GCG TGT GTG CTG TGG GTG
ala gly cys ala leu ser ala glu ser ser		arg thr leu leu ala cys val leu trp val	
3781/1261	CTG AAA AAC ACC GAG CCG GCG CTC CTG CAG	3811/1271	CGC TGG GCC ACT GAC CTG ACA CTC CCC CAG
leu lys asn thr glu pro ala leu leu gln		arg trp ala thr asp leu thr leu pro gln	
3841/1281	CTG GGA CGT CTG TTG GAC TTG CTG TAC CTT	3871/1291	TGC CTG GCT GCC TTT GAG TAC AAG GGG AAA
leu gly arg leu leu asp leu leu tyr leu		cys leu ala ala phe glu tyr lys gly lys	
3901/1301	AAG GCC TTT GAA CGC ATC AAC AGC CTC ACA	3931/1311	TTC AAA AAA TCT CTG GAT ATG AAG GCG CGG
lys ala phe glu arg ile asn ser leu thr		phe lys lys ser leu asp met lys ala arg	
3961/1321	CTA GAG GAA GCC ATT CTG GGT ACC ATC GGA	3991/1331	GCT CGA CAA GAA ATG GTT CGG CGA AGT CGT
leu glu glu ala ile leu gly thr ile gly		ala arg gln glu met val arg arg ser arg	
4021/1341	GAG AGG AGC CCG TTT GGG AAT CCA GAG AAC	4051/1351	GTG CGC TGG CGG AAG AGC GTC ACA CAC TGG
glu arg ser pro phe gly asn pro glu asn		val arg trp arg lys ser val thr his trp	
4081/1361	AAG CAA ACC TCA GAC CGC GTG GAC AAG ACC	4111/1371	AAG GAT GAA ATG GAA CAC GAG GCC TTG GTG
lys gln thr ser asp arg val asp lys thr		lys asp glu met glu his glu ala leu val	
4141/1381	GAA GGG AAC CTG GCA ACC GAG GCA AGC CTA	4171/1391	GTG GTT CTG GAC ACA CTG GAG ATC ATC GTG
glu gly asn leu ala thr glu ala ser leu		val val leu asp thr leu glu ile ile val	
4201/1401	CAG ACG GTG ATG CTT TCA GAA GCC CGG GAG	4231/1411	AGC GTC TTG GGG GCA GTG CTG AAG GTT GTG
gln thr val met leu ser glu ala arg glu		ser val leu gly ala val leu lys val val	
4261/1421	CTG TAC AGC CTG GGC AGT GCC CAG AGT GCC	4291/1431	CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG
leu tyr ser leu gly ser ala gln ser ala		leu phe leu gln his gly leu ala thr gln	
4321/1441	AGG GCC CTT GTG TCC AAG TTC CCG GAG CTG	4351/1451	CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC
arg ala leu val ser lys phe pro glu leu		leu phe glu glu asp thr glu leu cys ala	
4381/1461	GAC CTG TGC CTG AGG CTC CTA CGA CAC TGT	4411/1471	GCG AGC CGC ATC AGC ACC ATC CGC ACG CAC
asp leu cys leu arg leu leu arg his cys		gly ser arg ile ser thr ile arg thr his	
4441/1481	GCC AGC GCC TCG CTG TAC CTG CTC ATG CGA	4471/1491	CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC
ala ser ala ser leu tyr leu leu met arg		gln asn phe glu ile gly his asn phe ala	
4501/1501	CGT GTG AAG ATG CAG GTC ACC ATG TCT CTC	4531/1511	TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC
arg val lys met gln val thr met ser leu		ser ser leu val gly thr thr gln asn phe	
4561/1521	AGT GAA GAG CAC CTG CGA CGT TCA CTC AAA	4591/1531	ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG
ser glu glu his leu arg arg ser leu lys		thr ile leu thr tyr ala glu glu asp met	
4621/1541	GGG CTG CGG GAC AGC ACC TTC GCA GAG CAG	4651/1551	GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG
gly leu arg asp ser thr phe ala glu gln		val gln asp leu met phe asn leu his met	
4681/1561	ATC CTG ACG GAC ACG GTG AAG ATG AAG GAA	4711/1571	CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC
ile leu thr asp thr val lys met lys glu		his gln glu asp pro glu met leu ile asp	
4741/1581		4771/1591	

CTC ATG TAC AGA ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG
 leu met tyr arg ile ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu
 4801/1601 4831/1611
 CAG AAC ATG GCC GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG
 gln asn met ala gly lys his ala glu leu gly asn his ala glu ala ala gln cys met
 4861/1621 4891/1631
 GTG CAC GCG GCC GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAG CGC CAC CTG
 val his ala ala ala leu val ala glu tyr leu ala leu leu glu asp gln arg his leu
 4921/1641 4951/1651
 CCC GTG GGC TGC GTT TCC TTC CAG AAC ATC TCA TCC AAC GTG CTA GAG GAG TCC GCC ATC
 pro val gly cys val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile
 4981/1661 5011/1671
 TCC GAC GAC ATC CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG
 ser asp asp ile leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu
 5041/1681 5071/1691
 CTG GGG CTG GTA GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC
 leu gly leu val gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr
 5101/1701 5131/1711
 GAG GCG GTG AAT GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC
 glu ala val asn glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr
 5161/1721 5191/1731
 AAG AAG CTG GCC GCG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG
 lys lys leu ala ala val his gly lys leu gln glu ala phe thr lys ile met his gln
 5221/1741 5251/1751
 AGT TCC GGC TGG GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC
 ser ser gly trp glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his
 5281/1761 5311/1771
 TTC GGT GAC CTG GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA
 phe gly asp leu asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala
 5341/1781 5371/1791
 GAG ATC TCA CAC CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG
 glu ile ser his arg leu glu glu phe tyr thr glu arg phe gly asp asp val val glu
 5401/1801 5431/1811
 ATT ATC AAA GAC TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC
 ile ile lys asp ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile
 5461/1821 5491/1831
 CAG ATC ACG TAT GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC
 gln ile thr tyr val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr
 5521/1841 5551/1851
 TTT GAC CGC AAC TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG
 phe asp arg asn tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly
 5581/1861 5611/1871
 CGC GCA CAC GGG GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC
 arg ala his gly glu leu pro glu gln his lys arg lys thr leu leu ser thr asp his
 5641/1881 5671/1891
 GCC TTC CCC TAC ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG
 ala phe pro tyr ile lys thr arg ile arg val cys his arg glu glu thr val leu thr
 5701/1901 5731/1911
 CCA GTG GAG GTG GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC
 pro val glu val ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr
 5761/1921 5791/1931
 GAG CAG GAC CCA CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC
 glu gln asp pro pro asp ala lys met leu gln met val leu gln gly ser val gly pro
 5821/1941 5851/1951
 ACC GTG AAC CAG GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC
 thr val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp
 5881/1961 5911/1971
 CCC AAG CTC TTC CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA
 pro lys leu phe arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys
 5941/1981 5971/1991
 TGT GAG GAT GCG CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC

cys glu asp ala leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his
 6001/2001 6031/2011
 CGT GAG CTG GAG CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG
 arg glu leu glu arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln
 6061/2021 6091/2031
 CGC CTG CCC CAG CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA
 arg leu pro gln leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala
 6121/2041 6151/2051
 AGT TTC CGA AAG GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG
 ser phe arg lys ala asp leu OPA
 6181/2061 6211/2071
 CAC CCG GGC CTC AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT

 6241/2081 6271/2091
 GGG GTG ACC ACA CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA

 6301/2101 6331/2111
 CTG ATG CTT CCT CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-7 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1993	G to A; glycine to arginine
2	2136	A to G; missense
3	3166	A to G; threonine to alanine
4	3902	A to T; lysine to methionine
5	3918	C to T; missense
6	3937	A to C; lysine to glutamine
7	4002	A to C; glutamic acid to aspartic acid
8	4017	T to A; serine to arginine
9	4020	T to C; missense
10	4034-5	TT to AC; phenylalanine to tyrosine
11	4911	G to C change; missense mutation changing codon from glutamine to histidine

These differences may be found separately or together in various combination in the difference human CLASP-7 isoforms

FIG. 5

B

C

FIG. 5

CLASP-7 intron/exons

Exon 63800 to 63920

GCGGGGCGGGGCCCCGGGGCGGGCGGGCGGGGACGCGAGGACCATGGCTGC
CTCCGAGCGCCGCGCCTTCGCGCACAAAGATCAACAGGTAGTGTGGCCGCGGG
GCCCCCTCCACCTCCC

Exon 72530 to 72670

CCAATGGCCCCCTCCCTATCTTTCCAGGACGGTGGCCGCAGAGGTGCGGAAG
CAGGTGTCCCGGGAACGCAGTGGCTCCCCCCTCCAGCAGGCGCTGCAGCA
GCTCCCTGGGGGTAAGTATTTGGGGGGTCCGCCCCCA

Exon 73300 to 73530

TCACAGCCACTTTGCTCCAATCCAGGTCCCACTGACTGAAGTTGTCGAGCCCC
TGGACTTTGAGGATGTACTTCTGAGCCGGCCACCAGATGCTGAGCCCCGGGCC
CCTCAGGGACCTGGTAGAATTCCCAGCTGATGACTTGGAGCTGCTGCTGCAG
CCCCGGGAATGCCGGACCACGGAGCCCCGGGATCCCCAAGGATGAGTGGGTTC
AGCCCCACGCCCTCTCTGCCTG

Exon 73700 to 73830

GTCTCTGTTTACCCTGATCTTCTTTTGCTGCAGAAACTGGATGCCCAGGTGA
GGGCCGCGGTGGAGATGTATATTGAGGACTGGGTCATTGTCCACAGAAGGTG
AGTCTGACTTAGGGGCAGCTCAGGGG

Exon 74010 to 74190

CCTGCCCAGCCCCGTTTCCTGCTAGGTATCAGTACCTGAGTGCAGCATAACAGC
CCCGTCACCACAGACACACAGCGGGAGCGACAGAAGGGCCTCCCCCGCCAG
GTCTTTGAGCAGGATGCTTCTGGAGACGAGAGGTCCGGCCCTGAGGACTCGG
TGAGGAAGCCCCTGGCTGGGGTCAC

Exon 75170 to 75450

CAGTGCTTGACATTCTCCACTGGCAGAAATGACTCCCGGCGTGGCTCGGGCTC
CCCGGAAGACACCCCTCGAAGCAGTGGTGCCTCTAGCATCTTCGACCTGAGG
AACCTGGCAGCTGACTCATTGCTGCCCTCTCTGCTAGAGCGGGCGGCCCCAG
AAGATGTGGACCGGCGCAATGAAACCCTTCGACGGCAGCACCGGCCCCCGGC
CCTGCTCACCCCTCTACCCGGCACCTGACGAGGTGGGTGCCCTTCCCAGATAT
CAGCCAACCAGCATTACT

Exon 78100 to 78250

CCCGCCCAGCTCCCACCCCCCACTCTTGGCAGGATGAAGCCGTGGAACGCTG
TAGCCGCCAGAGCCACCCCGCGAGCACTTTGGACAAAGGATCTTGGTCAAG
TGTCTGTCGCTCAAGTGAGTATACTGACATGTCTCTCTTCTTAGATG

Exon 80380 to 80500

CCCCCTCCCTCCCATTACTTGTAGGTTTCGAGATTGAAATTGAGCCCATCTTT
GGGATCTTGGCTCTGTATGATGTGCGGGAGAAAAAGAAGGTAGGAGGCCCTT
TTTTCTCTTTCCTCCC

Exon 80540 to 80750

GTGGTGGCCCAGCTGCCTCTGGTGTCCCCAGATCTCGGAGAACTTCTACTTCG
ACCTGAACTCGGACTCCATGAAGGGGCTGCTTCGGGCTCATGGCACCCACCC
TGCCATCTCCACCCTGGCCCGCTCTGCCATCTTCTCTGTGACCTACCCCTCACC
TGACATCTTCCTGGTCATCAAGGTGCCTGCTGGGGCTGGGCAAGGGGGTGGT

Exon 82370 to 82510

GCCTCACTGGATTCATTCATCTGCCCCGCAGTTGGAGAAGGTGCTTCAGCAAG
GGGACATCAGTGAGTGCTGTGAGCCTTACATGGTGTGAAAGAAGTGGACAC
AGCCAAGGTAAGCGTGTGGAGGCTGGACTAGGGGCA

Exon 82540 to 82760

GCTGAGCTGGCAGGGGACGGGGTCTCCCCACAGAACAAAGAGAAGCTAGAG
AAGCTGCGCCTGGCGGGCCGAGCAGTTCTGCACCCGCGCTGGGCCGCTACCGCA
TGCCCTTCGCTGGACGGCCGTGCACTTGGCCAAACATCGTGAGCAGCGCTGG
GCAGCTGGACCGGGACTCTGACTCGGAGGGGCGGTTGAGGAGGCGGGGGCTAAC
AGGCTTGGGGCGGGG

Exon 82860 to 83060

CTTGGTCCCCCTTTTGTCAATTGTCATTCCCTCCCCTAGAGCGCCGGCCAGCCT
GGACAGACCGCCGCGCTCGGGGGCCCCAGGACCGGGCGAGTAGTGGGGACG
ACGCCTGCAGCTTCTCTGGCTTCCGTCCAGCCACGCTAACTGTCACAACTTC
TTTAAGCAGGTGTCCTACCCTGGGGCCAGGGACTCTCCCACTCC

Exon 83100 to 83260

GCCCAGGCTGACGGGAGTGGGTCCCATGTAGGAGGCTGAGCGACTCAGTGAC
GAGGACCTCTTCAAGTTCCTGGCTGACATGAGGCGCCCGTCGTCCCTGCTGCG
GCGACTACGTCCTGTGACTGGTGCCTGGCACACCCCATACACAAGAAGTATC
ACTC

Exon 84050 to 84270

GTGCAAACCGGTTCTTCCCTTCCCAGCCCAGCTCAAGATCGACATTTCTCCGG
CTCCTGAAAATCCCCACTTCTGCCTCTCCCCTGAGCTGCTTCATATCAAGCCC
TACCCGGACCCCAGGGGGCCGGCCACCAAGGAGATTCTGGAGTTCCCCGCCC
GCGAAGTCTATGCCCCCATACCAGCTACAGGTACGGCCTCTGGGGCCCAGC
TGGGCACTTGA

Exon 87940 to 88130

GCCCCGTGTCCTCTGACACCCCCATCCTGCCCCCACAGGAACCTGCTGTACG
TGTACCCGCACAGCCTCAACTTCAGCAGCCGCCAGGGCTCCGTGCGCAACCT
TGCTGTGCGAGTGCAGTACATGACAGGCGAGGACCCCAGCCAGGCTCTGCCG
GTCAGTGGCTGTGCCCCAGGGAAGGGGGGTAGGG

Exon 88140 to 88270

TGGGTCCCTCATGAATCCACTCTCCCAGGTCATCTTTGGCAAGTCCAGCTGCA
GTGAATTTACCCGCGAGGCCTTCACACCGGTGGTCTACCATAACAAGTATGT
AGGGGGACACGTGAGGAACCTTGGGGG

Exon 88470 to 88680

GCCCCCAGCAGATCCCCCAGCCCGATTCTGCCAGGTCCCCCGAGTTCTACGA
GGAGTTCAAGCTGCATCTTCCAGCCTGCGTGACAGAGAACCATCACCTGCTG
TTACCTTCTACCATGTGAGCTGCCAGCCCCGGCCGGGCACTGCCCTGGAGAC
ACCCGTGGGCTTTACTGTGAGCCGTCCCCTCCCTCCCTCCCCCTGAGCCCTCC
T

Exon 88680 to 88870

TCGTCCCCCAACCTGGCCGCAGACCTGACCTCCAGCCTCTCCCCAGTGGATCC
CACTGCTGCAGCACGGGCGCCTGAGGACCGGCCCTTCTGTCTCCCAGTGTCT
GTGGACCAGCCGCCGCCAGCTATTCCGTGCTCACACCCGATGTATGTGCCCT
GGAGCTCCTGCCTGCCAATGCACTGTCCCCAG

Exon 89360 to 89530

CAGGGAGGGCTGACCAGTGCCACCTGGTGCCTCCCTCCCACAGGTGGCGCT
TCCGGGCATGCGCTGGGTGGACGGTCACAAGGGCGTGTTCAAGTGTGGAGCTC
ACAGCCGTGTCTCTGTGCACCCCCAGGTACGGGGTGGGCCGGGAACCAAGA
GTCCCGCCCTGCTCC

Exon 89660 to 89980

TTCATTCCCTGAGGCCCCACCCTGCTCACTCCACATCCCTACCCAGGACCCCT
ACCTGGACAAATTCTTCACCCTGGTGCACGTCCTGGAGGAGGGAGCCTTCCC
ATTCCGGCTCAAGGACACTGTGCTGAGCGAGGGCAACGTGGAGCAGGAGCTG
CGGGCCAGTCTTGACGACTGCGCCTGGCCAGCCCCGAACCCCTTGTGGCCTT
CTCCCACCACGTGCTGGACAAGCTCGTTCGTCTGGTCATCAGGCCCCCGATC
ATCAGTGGCCAGATTGGTAAGCGAATGTGGCCTCAGACCTCAGTTTCCCCATC
CACATG

Exon 90480 to 90730

AGAGGCCTTGGGGCCCTGGAACCTTGACCTCTGCTCTGCCCTGCAGTGAACCTG
GGCCGTGGAGCCTTTGAAGCAATGGCCCATGTAGTCAGCCTTGTTACCCGGA
GCCTGGAGGCAGCCCAGGATGCCCGCGGTCACTGCCACAGCTGGCTGCCTA
CGTCCACTACGCCTTTCGCCTTCCTGGCACTGAGCCCAGCCTCCCGGATGGTG
AGTTTGTAGAAATCCCTGTGAGACGAGAAATATCTGGGAGAA

Exon 92870 to 93120

ATCACATCAGGTGGGTGGGTGGTTGACCCTATTCACTCCATCCTCAGGGGGCCC
CTCCAGTGACAGTGCAGGCTGCCACACTGGCCCGTGGCTCTGGTCGCCCCGC
AAGCCTCTACCTGGCGCGTTCCAAGAGCATCAGCAGCAGCAACCCTGACCTC
GCCGTGGCCCCCTGGCTCTGTGGATGACGAGGTTTCCCGCATCCTGGCCAGCA
AGGTAGGGCAACGGGGGGCCCTGGAATCTCCAGCCTCAGTGGT

Exon 97210 to 97390

GGCACCTCGCACTCTGTGACCCCTGCCTCTGTCCCCAGCTGCTTCACGAGGAG
CTGGCTCTGCAGTGGGTGGTCAGCAGCAGTGCCGTACGCGAGGCCATCCTCC
AGCACGCCTGGTTCTTCTTCCAGCTCATGGTGAGACCCCCTCCTCCCTGCCTG
GTGGCAAGAGACCCCCAGTGGAG

Exon 98770 to 98990

CAAATCCCACCCACAGCCCTCTACCCCCACCCCCAGGTGAAGAGTATGGCGC
TGCACCTGCTGCTTGGCCAGCGACTAGACACACCCCGCAAGCTGCGCTTCCC
CGGACGCTTCCTGGACGACATCACTGCCTTGGTGGGCTCTGTGGGCCTGGAG
GTCATCACCCGTGTCCACAAGGTGAGAGATGCAGGGTCTCAATGTGGGAAGA
AACCTGAGGGAGG

Exon 103130 to 103340

GGGGCTGAGGTTTGGGTGTGTGGGTGACAGGCACCTGTGTCCCCAGGATGT
GGAGCTGGCCGAGCACCTCAACGCCAGCCTGGCTTTCTTCCTCAGTGACCTTC
TGTCCCTGGTGGACCGGGGCTTTGTCTTCAGCCTGGTCCGGGGCCCACTACAAG
CAGGTAGGAGTGGGCGTGGGCAGGGTGGGCATGGCATGGATGGAAGGCGGA
GC

Exon 103340 to 103590

CAATGTTGACATCACTGATGGCCACCCCTCTCCTGCAGGTGGCCACGCGGCTC
CAGTCGTCCCCCTAATCCAGCAGCCCTGCTGACCCTGCGCATGGAATTCACCCG
CATCCTGTGCAGCCACGAGCACTACGTGACCCTCAACCTCCCCCTGCTGCCCCC
TGTCACCTCCAGCCTCGCCCTCCCCCTCTGTGTCCTCCACCACCTCCCAGGTG
GGCTGCCTTCACTTCTGCCTCCTCTCTTTGACCTACAAC

Exon 103990 to 104220

TGACCCTTGACCGCTGGCATCCCCCATTTTTCCCCCACTCTGCAGAGCTCCAC
CTTCTCCAGCCAAGCCCCGGACCCCAAGGTGACCAGCATGTTCTGAAGT
GGACCATTCGGGAGCAGCACTTCCTAGCTGGGCTCCTGCTGACGGAGCTGG
CACTGGCCCTCGAACCTGAGGCTGAAGGGTGAGCAGAGCTCCTGTCTAGCCC
CAGGACAGGTGGGACAGTCCAG

Exon 104220 to 104480

GGAGCCATGTCCACCCTGTCCTGAGCACCTCATTACCCCATAGGGCATTCCCTG
TTGCACAAGAAGGCCATCAGTGCTGTGCACAGCCTGCTATGTGGCCATGACA
CTGACCCCCGCTACGCCGAGGCCACTGTGAAGGCTCGTGTGGCCGAGCTGTA
CCTGCCACTGCTATCGATTGCACGGGATACCTTGCCACGGCTGCATGACTTTG
CTGGTCAGTGGGCCAGGGGAAGATGGGGTCACATGATCCAGGGACTTGGTC

Exon 108850 to 109100

ACCAAGGGTTTATCTTTCTTTCCCTCTGTCTTTCCCTGCCAGAGGGCCCAGGTC
AGCGGTCAAGACTGGCCTCAATGCTTGACTCAGACACAGAAGGCGAAGGGG
ACATTGCGGGTACCATCAACCCCTCTGTGGCCATGGCCATTGCTGGTGGCCCC
CTAGCCCCCTGGCTCCCGGGCCAGCATCTCCAGGGGCCACCAACGGTGAGTA
GGGAGGCTTGTCCCCATAGACATCATCCACTTTGAATGAGA

Exon 109140 to 109410

TCACATGGAGAAAATGGAAATTGACTTTGATTCTCTCTGGCCCCAGGCTTCT
CGCGCAGGCTGTGCCCTCTCTGCTGAGTCAAGCCGGACCTTGCTGGCGTGTGT
GCTGTGGGTGCTGAAAAACACCGAGCCGGCGCTCCTGCAGCGCTGGGCCACT
GACCTGACACTCCCCCAGCTGGGACGTCTGTTGGATTTGCTGTACCTTTGCCT
AGCTGCCTTTGAGTACAAGGTTTGAGGGCGTGCGCAGGAGATGATGGAGGAG
GCAGGCTA

Exon 110310 to 110530

GAAAAGAGCAGAGTCAGCCTGGAACCCCAAGTTCTCTGCACCCCCAGGGGAA
AAAGGCCTTTGAACGCATCAACAGCCTCACATTCAAAAAATCTCTGGATATG
AAGGCGCGGCTAGAGGAAGCCATTCTGGGTACCATCGGAGCTCGACAAGAA
ATGGTTCGGCGAAGTCGTGGTAAGAGGGTGACATACCCACGTGTCCCCATCC
CACCAGCTGCTCCCA

Exon 110770 to 110940

TGTGTTTTTACGCATCTGTGATCGTGACCCACGCGTCTCAGAGAGGAGCCCG
TTTGGGAATCCGGAGAATGTGCGCTGGCGGAAGAGCGTCACACACTGGAAGC
AAACCTCAGACCGCGTGGACAAGTAGGTGTGGGCAGGAGGGTGTCTGCTGAG
TTCAGAACAGTTTG

Exon 111590 to 111770

ATCTCACCCCGAGTGGGCCCCCAAGACCTCCTTTCCCCTTCCAGGACCAAGG
ATGAAATGGAACACGAGGCCTTGGTGGAAGGGAACCTGGCAACCGAGGCAA
GCCTAGTGGTTCTGGACACACTGGAGATCATCGTGACAGGTAGGGCTTGATCC
AGCATCTGCCTTGTGCTCTGAGCCCA

Exon 111830 to 112050

ACCCTAGGCTCTAACACCTGGATTTCTGACCCCTTCCCTCCAGACGGTGATG
CTTTCAGAAGCCCCGGGAGAGCGTCTTGGGGGCAGTGCTGAAGGTTGTGCTGT
ACAGCCTGGGCAGTGCCCAGAGTGCCCTCTTCTTGACAGCATGGCCTGGCCAC
CCAGAGGGGCCCTTGTGTCCAAGGTGAGCACCCTCAACAACCATGATTCTTA
GAAAAACAGTAG

Exon 112910 to 113140

AACGGGGAGGGGCTGGACAGTGTCTGTCTGGGTCTTGGGGGCAGTTCCCGG
AGCTGCTGTTTCGAGGAGGACACGGAGCTGTGTGCCGACCTGTGCCTGAGGCT
CCTACGACACTGTGGCAGCCGCATCAGCACCATCCGCACGCACGCCAGCGCC
TCGCTGTACCTGCTCATGCGACAGAACTTCGAGATCGGCCACGTGAGTGGGG
GCTAGGAGGCATGGTCCACACATGGCTCTGGTC

Exon 114090 to 114340

TCTGAGACTCCCGGCTCCACCCTCCCGCCCCCTGTCCCTGCAGAACTTTGCCCG
TGTGAAGATGCAGGTCACCATGTCTCTCTCGTCCCTGGTGGGGACGACGCAG
AACTTCAGTGAAGAGCACCTGCGACGTTCACTCAAAACCATCCTCACCTATG
CTGAGGAGGACATGGGGCTGCGGGACAGCACCTTCGCAGAGCAGGTGACAC
CTGCTGGGTCCCCGCCCCGCCTCCCCTTCATATAACTCCCAAC

Exon 114370 to 114550

ATGCTCTCATTGGCCCCCTGGACGTTCCCCGGCTCCAGGTCCAGGACCTGATGT
TCAACCTGCACATGATCCTGACGGACACGGTGAAGATGAAGGAACACCAGG
AGGACCCTGAGATGCTCATCGACCTCATGTACAGGTGAGGTGGGCCAGCTGG
CACCTTCAGCCACGCCCACGCCCA

Exon 116900 to 117170

AGGTGAGTCCCCTCCTCACATCCCCCCTCACCTGGACTCCAGAATTGCCCGGG
GCTACCAGGGCTCACCGGACCTTCGGCTGACCTGGTTGCAGAACATGGCCGG
GAAGCACGCGGACGTGGGCAACCACGCCGAGGCCGCCAGTGCA
CGCGGCCGCCCTCGTGGCTGAGTACCTCGCCCTGCTCGAGGACCAGCGCCAC
CTGCCCCGTGGCTGGCGATTTCTTCCAGGTGAGTGGCCAGGGGTTGGCAGGT
GGCGGACGGCA

Exon 117170 to 117410

ACGAGTGCAGTGGGGACCAGGGTCTGACGCCACCTCTCCACCCCAGAACAT
CTCATCCAACGTGCTAGAGGAGTCCGCCATCTCCGACGACATCCTGTCGCCC
GACGAGGAGGGCTTCTGCTCCGGGAAGCACTTCACTGAGCTGGGGCTGGTAG
GGTTGCTGGAACAGGCAGCCGGCTACTTCACCATGGTGAGGCCTTGGGGACT
GGGTGCAGGAGAGGGGGCTCGGGCCAGGGAGGT

Exon 121670 to 121900

GAGAGGAAGACAGTTTGGGGAATCCTGACCCACCTCACCTCAGGGCGGGC
TCTACGAGGCGGTGAATGAGGTCTACAAGAACCTCATCCCCATCCTGGAAGC
CCACCGTGACTACAAGAAGCTGGCCGCGGTGCACGGCAAACCTGCAGGAGGC
CTTCACCAAGATCATGCACCAGGTGGGCCAGGACCCCTCCCCAGACCCA
CCCTCAGCCCCACTCCTCATCC

Exon 121910 to 122000

CCCCAGGGATCTGCTGACCTTGACCCTTCTCTTCCCCACAGAGTTCGGCTGG
GAGGTGAGTCAGCCTTGGTGGACAGCCACCTGCCTCTG

Exon 123290 to 123510

TCCAGCAGGGGCCTCCCGGACAACCACACCCTTTCTCACAGCCCCAGCGCGT
GTTTCGGGACGTATTTCCGCGTGGGCTTCTACGGCGCCCACTTCGGTGACCTGG
ATGAGCAGGAGTTTGTGTACAAGGAGCCATCGATCACGAAGCTGGCAGAGAT
CTCACACCGGCTGGAGGCATGTCCTTGTGGTTGGGGGTGGAACGGGGCATGG
GGCTGCCTTGGG

Exon 123510 to 123633 (end clone)

GGCTGGAGTAGGGGCTGTCCCTGGGTGGCCCCGAGTCAGCCCTGTGTCTCCA
GGAGTTCTACACGGAGAGATTTGGCGACGACGTCGTTGAGATTATCAAAGAC
TCTAACCCCTGTGGACAAGTC

Human CLASP-7 promoter region , 61938 (beginning of contig) to 63888 (end of first predicted exon)

GGGCATGTGGCTCATTCTGTAATCCCGGCACTTTGGGAGGCCGAGGCGGGTGGATC
ACCTGAGGTCAGGAGCTCCAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTAC
TAAAAATACAAAAAATTAGCCAGGTGTGATGGTGGGTGCCTGTAATCCCAGCTACTC
GGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCAGAGGTTGCGGTGAGCC
GAGATTGTGCCATTGCACTCCAGTCTGGGCAACAAGAGCGAAATGCCACCTCAAAAT
AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAGAGGATAA
AATGCCAGCAACCCATAGATGGGAATGAGAACAGCACGTGCAAAGGCCCTGAGGCA
GAGCCACGGCCTTGTCTGATTCAACCTCAAATTCTCCCTGGGGCATTGTCTGACCAGG
GAAAGAAGGGCTGTCCAGGAGGAAGGACCTGCCGGTGCAGAGGCATGCAGGTGAGA
AAGGGGTGAGCTCCTCCAGAGGGGAGTGTGCGCTGGAGAATTCTCTAAAAATGCTGC
AGCAGTGCTGGGAGAGAGGCCAGTGGGGAGAGATTTGAGACCATAGATTAACCAAG
ACATCCCCACCTCTTCTCTTGGTAGAGGCGGCCCGAAAGTCTAGACTCCCAAAT
GGCTCACTCAGGTCCCACCACCTGGACCTGGGGCACATCTCCGAGCACTCCAGTGCC
TAGCCAGGCTCCTCTGACTCCCATGCTGTAGACTGGGAGCACGGACAATGCAGGGCGC
TGGAGACCCCTGTGAGTCACACTGAGCAAGCACCCGAACACCTCTGTGCCTCAGTTT
ACTCATCTGTAAAAGGAGGAAAACAATAATTTCTTCTGCATGTGTGAATTGCAGGGC
CAGGCTCAATGACATCTTAGCAATTAGACTTTTTGAGACAGGGTCTCGCTCTGTCAAC
CAGGCTGGATTGAAATGGCACAATCACAGCTCACTGCAGCCTTGACCTCCCAGGCTC
AAGCGATCCTCCTCCCTCAGACTCCCAAGTAGCTGAGATTACAGGCACACACCACCA
TGCCTGGTTAATTTTTGCATTTTTGTGGACACGGGGTCTCATTATGTTGCCAGGCT
GGTCTCCAACCTCCTGGGCTCAAACAATCCTCCTGCCTTGGCCCCCACAGTGCTGGG
ATTACAGGCATGAGCCACCATGCACGGCCACGATTATACTTACAGGTATGATTATTA
GATACATGAACATCGTTATTGTTTTCCAGCCAGGAGTCAGAGGGCAGAAAGAGCGCC
CCCCAAACCCCGGAAATCTGGGGCCTACCCAGCCTGGGTCCAGCGCCTCCCCTCCC
TCCCTCCCTCCTGAGCTTCAGTTTCCCCAGCCCTGCTCCTGGGGTGGTAAGACCACCC
CACTAAACCCCGGGAGCCTGGGGTCCACCTAGCCCGGGTCTCAGCGCCTCCCTTCCC
TCCCTCCCTCCTCAGGCTCAGTTTCTCCAGCCCAGCTCCAGGGTGGAAAGAGCGCC
CCCGCCAGCTCGGGAGTCTGGGGCACCCCCAGTCTGGGTCCAGCGCCTCCTCTCCC
TAACTTCCCTCCTCAGCCTCAGTTTCCCCAGCCCTTCTCCTAGGGTAGAAAGAGCGTC
CCCCCAGCCCGGGAGTCTGGGGCCCCGCCAGCCTGGATCCCGGGGCCTCCTCTCCGT
CCCCAGCCTCAGTTTCCCCAGCCCCCAGGACTCCAGGCGACCCCTCCGGCCTGCAGG
GGCAGCACGGAGCGGCCCGGGCCACCCGGAAGGGCCCCCGCCCCGCGCCGGCCCCG
CCCCGCCCCGGCTGCCAGAACCGGGAGGCGGGCGGGCGGGGCGGGGCCCCG
GGGCGGGCGGGCGGGACGCGAGGACCATGGCTGCCTCCGAGCGCCGCGCCTTCGC
GCACAAGATCAACAGG

FIG. 6

hCLASP4	-----MFPMEDISISVIGRQRTVQ-----	20
hCLASP5	-----MTHLNSLDVQLAQELG-----	16
hCLASP3	-----MAERRAFAQKISRTVAAEVKQISGQYSGSPQLLKNNLIVG	41
hCLASP2	-----MLLFPYDDFQTAILRRQGRIYS-----	23
hCLASP7	-----MAASERRAFAHKINRTVAAEVKQVSRERSGSPHSSRRCSSSL	43
hCLASP1	MSFRGKVFKEPSEFWKKRRTVRRVIOEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN	60
...		
hCLASP4	-----STVPEDA EKRAQSLFVKECIKTYSTDWHVVNYK	53
hCLASP5	-----DFT	19
hCLASP3	N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP	83
hCLASP2	-----TVPKAE EEAQSLFVTECIKTYNSDWHLVNYK	55
hCLASP7	G-----VPLTEVVEPLDFEDVLLSRPPDAEPGRLRDLVEFP	79
hCLASP1	DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDA EHKAEENLLVKEACKFYSSQWHVVNYK	120
::		
hCLASP4	YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG	105
hCLASP5	DDDL DVVFTPKCRTLQP-SLPEEGVELDPHVR-----DCVQTYIREWLI	63
hCLASP3	PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI	126
hCLASP2	YEDYSGEFRQLPNKVVKLDKLPVHVYEVDEEVDKDED-----AASLGSQKGGITKHG	107
hCLASP7	ADDLELLLPRECRTEP-GIPKD-EKLD AQVR-----AAVEMYIEDWVI	122
hCLASP1	YEQYSGDIRQLPRAEYKPEKLPSHSFEIDHEDADKDEDTTS HSSSKGGGGAGGTGVFKSG	180
:: . * . :: .		
hCLASP4	WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDGSYILNSYKDEKNSKESK-GCIYLDACI	162
hCLASP5	VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHLNVLC	118
hCLASP3	VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPD GNSYQDDQDDLKR SMSI	183
hCLASP2	WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSYNLNFYKDEKISKEPK-GSIFLDSCM	164
hCLASP7	VHRRYQYLSAAY--SPVTTDTQRERQKG-LPRQVFEQDASGDERSGPEDSND SRRGSGSP	179
hCLASP1	WLYKGNFNSTVNNTVTVR SFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLD SCT	239
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hCLASP4	DVVQCPKMRRHAFELKMLDKYSHYLA AETE QE ME EW LITLKKIIQINTDSL VQEKKETVE	222
hCLASP5	DVSGKG PVTACDFDLRSLQPDKRL ENLLQQVSAEDFEKQNEEAR TN-----RQAE	169
hCLASP3	DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRONDDQRKSN-----RHKE	234
hCLASP2	GVVQNNKVRRAFELKMQDKSSYLLAADSEVEME EWITILNKILQLN-----FEAAMQEK	219
hCLASP7	EDTPRSSGASSIFDLRNLAADSL LPSLLERAAPEDVDRRNETLRRQH-----RPPA	230
hCLASP1	GVVQNNRLRKYAFELKMNDLTYFVLAAETESDMDEWIHTLNRILQISPEGPLQGRSTEL	299
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hCLASP4	TAQDD ETSS-----QGKAENIMASLERSMHP ELMKYGRETEQLNKLSRGDGRQNLFSFDSE	278
hCLASP5	LFALYPSVD-----EEDAVEIRPVPEC PKEHLG-----N-----RILVKLLTLKFEIE	212
hCLASP3	LFALHPSPD-----EEPIERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE	277
hCLASP2	RNGDSHEDD-----EQSKLEGSGGLDSYLP ELAKSAREAEIK---LKSES RVKLFYLDPD	272
hCLASP7	LLTLYPAPD-----EDEAVERCSRPEPPREHFG-----QRI LVKCLSLKFEIE	273
hCLASP1	TDLGLDSL DNSVTCECTPEETDSS ENNLHADFAKYLTETEDTVKTTNRMERLNLFSLDPD	359
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hCLASP4	VQRLDFS-----GIEPDIKP-FEEKCNK RFLVNCHDLTFN ILGQIGDNAKG PPTNVEPFFI	333
hCLASP5	IEPLFAS-----IALYDVKERKKI SENFHC DLNSDQFKGFLRAHTPSVAASSQARS AVFSV	268
hCLASP3	IEPIFAS-----LALYDVKEKKKI SENFYFDL NSEQMKGLLRPHVPPAAITTLARSAIFSI	333
hCLASP2	AQKLDFS-----SAEPEVKS-FEEKFGKRI LVKCN DLSFNLQCCVAENE EGPTTNVEPFFV	327
hCLASP7	IEPIFGI-----LALYDVREKKKI SENFYFDLNSDSMKGLLRAGTHPAISTLARSAIFSV	329
hCLASP1	IDTLKLQKDLLEPESVIKPFEEKAAKRIMI ICKALNSNLQGCVTENENDPITNIEPFFV	419
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FIG. 7
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Cadherin EC motif

hCLASP4	PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGI	LLRETSI	1060
hCLASP5	FFMNADTAPTSP--CPSISSQSSSSCSFQDQKIASMFDLTSEYRQOHFLTGI	LFTELA	1085
hCLASP3	PCSLLTTPASPSPSVSSATSQSSGFSTNVQDQKIANMFELSVPFROQHLAGI	VLTELAV	1196
hCLASP2	PMPFGKGRIQR-----YQDL--QLDYSLTDEFCRNHFLVGI	LLREVGT	1052
hCLASP7	PCCPLSPASPSPSVSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQOHFLAGI	LLTELAL	1119
hCLASP1	PIRSANIPDPLTP-----SES-----TQELHASDMPEYSVTNEFCRKHFLIGI	LLREVGF	1157
		..: : : : * * : : *	
hCLASP4	ALQDN----YEIRYTAISVIKNLLIKHAFDTRYQHKNQAKIAQLYLPFVGLL	ENIQR	1116
hCLASP5	ALDAEGEGISKVQRKAVSAIHSLLSSHDLDPKVCPEVKVKIAALYLPVGI	ILDALP--	1143
hCLASP3	ILDPDAEGLFGLHKKVINMVHLLSSHSDSPRYSDPOIKARVAMLYLPLIGI	IMETVP--	1254
hCLASP2	ALQEFR----EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGL	LIENVORI	1108
hCLASP7	ALEPEAEGAFILHKKAISAVHSLLCGHDTDPRYAEATVKARVAELYLPLLS	IARDTLP--	1177
hCLASP1	ALQEDQ----DVRHLALAVLKNLMAKHSFDDRYREPRKQQAQIASLYMPLY	GMLLDNMPRI	1213
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hCLASP4	AGRDTLYSCA-----AMPN-S---ASRDEFP CGFTSPANRGSLS	TDKDTAYGS	1160
hCLASP5	-----QL-----CDFTVADTRRYRTSGSD-----		1162
hCLASP3	-----QLY-----DFTETHNQGRPICIA	TD--	1276
hCLASP2	NVRDVSPFPVNAGMTVKDESALPA-VNPLVTPQKGSTLDNSLHKDLLGAIS	GIASPYTT	1167
hCLASP7	-----RLH-----DFAEGPGQRSRLASMLDS	TE	1201
hCLASP1	YLKDLYPFTVNTSNQGSRDDLSNNGGFQSQTAIKHANSVDTSFSKDV	LNSIAAFSSIAIS	1273
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hCLASP4	FQ-NGHGIKREDSRGS LIPEGATGFDPQNGTGEN-----TRQSSTRSSVS	QYNRLDQYE	1213
hCLASP5	-----EEQEGAGAINQNALAIAGNNENLKT-----SGIVLSSLPYKQY	NMLNADT	1208
hCLASP3	-----YESEGSMISQTVAMAIAGTSVPQLTR-----PGSFLTSTSGRQ	HTTFAES	1324
hCLASP2	STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSSTLGNSV	VRCDKLDQSE	1227
hCLASP7	-----GEGDIAGTINPSVAMAIAGGPLAPGSR-----ASISQGPPTAS	RAGCALSAES	1249
hCLASP1	-----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIG	STLRFDRLDQAE	1327
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hCLASP4	IRSLLMCYLYIVKMISEDTLLTYWNKVSPOELINILILLEVCLFHFRYM	GKRNIA RVHDA	1273
hCLASP5	TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYK	GKQSSDKVSTQ	1268
hCLASP3	SRSLICLLWLKNADETVLQKWFTDLSVLQNLRLDLLYLCVSCFEYK	GKKVFERMNSL	1384
hCLASP2	IKSLLMCFYILKSMSDDALFTYWNKASTSELMDDFFTISEVCLHQFY	QYMGKRYIARNQEG	1287
hCLASP7	SRTLLACVLWLKNTEPALLQRWATDLTLPQLGRLLDLLYLCLAAFEY	GKKKA FERINSL	1309
hCLASP1	TRSLLMCFHIMKTISYETLIAYWQRAPSPESVDFFSILDVCLQNF	RYLGKRNIRKIAA	1387
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hCLASP4	WLSKHFGIDR-----KSQTMPALRNRSQVMQARLQHLSSLESS-----		1311
hCLASP5	VLQKSRDVKAR-----LEEALLRGE GARGEMMRRRAPGNDRFPGLNEN---		1311
hCLASP3	TFKKS KDMRAK-----LEEAILGSIGARQEMVRRSRGQLERSPSGS	AFGSQ	1430
hCLASP2	LGPIVHDRKS-----QTLPVSRNRTGMMHARLQQLGSLDNS-----		1323
hCLASP7	TFKKS LDMKAR-----LEEAILGTIGARQEMVRRSRERSPF	GNPEN	1350
hCLASP1	AFKFVQSTQNNGT LKGSNPSCQTSGLLAQWMHSTSRHEGHKQHR	SQTLPIIRGKN	1442
	. : . : . :		
hCLASP4	-----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISF	FOCFKTQLL	1359
hCLASP5	--LRWKKEQTHWRQANEKLDKTKAE L DQEALISGNLATEAHLIILDMQENI	QASS-ALD	1368
hCLASP3	ENLRWRKDMTHWRQNT EKLDKSRAEIEHEALIDGNLATEANLIILDTLEI	VQTVS-VTE	1489
hCLASP2	-----LTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLE	FLAFKNQLL	1371
hCLASP7	--VRWRKSVTHWKQTS DRVDKTKIEMEHEALVEGNLATEASLVVLD	TEIIVQTVM-LSE	1407
hCLASP1	--ALSNPKLLQMLDNTMTSNSNEIDIVHHVDTEANIATEGCLTIL	DVLSLETQTHQRQLQ	1500
	. : : . * * * * * .		

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hCLASP4 NNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFISKFPFAFFKGRVNMCAAFCY 1419
hCLASP5 CKDS---LLGGVLRVLVNSLNCDSSTTYLTHCFATLRALIAKFGDLLFEEVEQCDFDLCH 1425
hCLASP3 SKES---ILGGVLKVLLHSMACNQSAVYLQHC FATQRALVSKFPELLFEEETEQCADLCL 1546
hCLASP2 ADHGHNPMLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRADMCALCY 1431
hCLASP7 ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQRALVSKFPELLFEEDTELCADLCL 1464
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLFVCKFPFAFFQGPADLCGSFCY 1560
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hCLASP4 EVLKCCTSKISSTRNEASALLYLLMRNFEYTKRKTFLRTHLQII IAVSQLIADVALSGG 1479
hCLASP5 QVLHHCSSSMDVTRSQACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483
hCLASP3 RLLRHCCSSSIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSLSSLVGTSQNFNE 1604
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTHLQVII SVSQLIADVVGIGE 1491
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGTTQNFSE 1522
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSQLIADAG-IGG 1619
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hCLASP4 SRFQESLFI INNFANS DRPMKATAFPAEVKDLTKRIRTVLMATAQMKHEKDPPEMLIDLQ 1539
hCLASP5 EHLRRSLRTILAYSEEDTAMQMTFFPTQVEELLCNLSILYDTVKMREFQEDPEMLMDLM 1543
hCLASP3 EFLRRSLKTILTYAEDLELRETTFPDQVQDLVFNLMILSDTVKMKEHQEDPEMLIDLQ 1664
hCLASP2 TRFQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKHEHNDPEMLVDLQ 1551
hCLASP7 EHLRRSLKTILTYAEDMGLRDSTFAEQVQDLMFNLHMILTDTVKMKEHQEDPEMLIDLQ 1582
hCLASP1 SRFQHS LAITNNFANGDKQMKNSNFPFAEVKDLTKRIRTVLMATAQMKHEKDPPEMLVDLQ 1679
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transmembrane

hCLASP4 YSLAKSYASTPELRKTWLD SMAKIHVKNGDFSEAMCYVHVAALVAEFLHRKK----- 1592
hCLASP5 YRIAKSYQASPDRLRLTWLQNM AEKHTKKKQYTEAMCLVHAAALVAEYLSMLEDH----- 1598
hCLASP3 YRIAKGYQTSPE-RLTWLQNMAGKHSERSNHAEEAQC LVHSAALVAEYLSMLEDH----- 1718
hCLASP2 YSLAKSYASTPELRKTWLD SMARIHVKNGLLSEAMCYVHV TALVAEYLTRKG----- 1604
hCLASP7 YRIARGYQGPSDLRLRLTWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYI ALLEDQ----- 1637
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGLLSEAMCYIHIAALIAEYIKRKG YWKVEKI 1739
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hCLASP4 -----LFPNGCSAFKKITPNIDEEGAMKEDAGMMD----- 1622
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVVS EDTLSPDEGVDV 1633
hCLASP3 -----KYLPGVCVTFQNISSNVLEESAVSDDVVS PDEEGI 1753
hCLASP2 -----VFRQGCTAFRVITPNIDEEASMMEDVGMQD----- 1634
hCLASP7 -----RHLPVGCVSFQNISSNVLEESAISDDILSPDEEGF 1672
hCLASP1 CTASLLSEDTHPCDNSNLLTTPSGGSMFSGWPAFLSITPNIKEEGA AKEDSGMHD----- 1795
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ITAM

hCLASP4 ---VHYSEEVLLELLEQCVDGLWKAERYEII SEISKLVPIYIEKRREFEKLTVYRTIHG 1679
hCLASP5 CAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIP ILEAHREFRKLTLTHSKLQR 1693
hCLASP3 CSGKYFTESGLVGLLEQAAASF SMAGMYEAVNEVYKVLIP IHEANRDAKKLSTIHGKIQE 1813
hCLASP2 ---VHFNE DVLME LLEQCADGLWKAERYELIADIYKLIPIYIEKRR----- 1677
hCLASP7 CSGKHFTELGLVGLLEQAAGYFTMGGLYEAVNEVYKNLIP ILEAHRDYKKLA AVHGKIQE 1732
hCLASP1 ---TPY NENILVEQLYMCGEFLWK SERYELIADV NKP IIAVFEKQ RDFKKLSDIYYDIHR 1852
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ITAM DOCK motif DOCK motif ITAM

hCLASP4 AYTKILEVMHTKKRLLGTF FRVAFYQG SFFEEEDGKEYIYKEHKL TGLSEISRLV KLYG 1739
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGEFG-SKFGDLDEQE FVYKEHAITKLPEISRLEAFY G 1750
hCLASP3 AFSKI VHQSTGWERMFGTYFRVGEY G-TKFGDLDEQE FVYKEHAITKLAEISRLEGFY G 1872
hCLASP2 -----DFFEDEDGKEYIYKEHKL TPLSEISORLLKIYS 1710
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGEY G-AHFGDLDEQE FVYKEHSITKLAEISRLEEFYT 1791
hCLASP1 SYLKVAEVVNSEKRLFG RYRVAFYQG SFFEEEDGKEYIYKEHKL TGLSEISORLLKIYA 1912
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	ITAM	ITAM	
hCLASP4	EKEFGTENVKIIQDSDKVNAKELDPK	YAHYIQVTVVKHYFDDKELTERKTEFERNHNISRFV	1799
hCLASP5	QCQGAEFVEVIKDSPTVDKTKLDPN	KAYIQITFEVEHYFDEYEMKDRVTYFEKNFNLRRFM	1810
hCLASP3	ERFEGEDVVEVIKDSNPVDKCKLDPN	KAYIQITFEVEHYFDTYEMKDRITYFDKNYNLRRFM	1932
hCLASP2	DKFGESENVKMIQDSGKVNPKDLDSK	YAYIQVTHVHFFDEKELQERKTEFERSHNIRRFM	1770
hCLASP7	ERFGDDVVEIIKDSYPVDKSKLDSK	KAYIQITFEVEHYFDTYELKDRVTYFDRNYGLRTFL	1851
hCLASP1	DKFGADNVKIIQDSNKNVPKDLDPHY	YAYIQVTVVTFEFEEKEIEDRKDTDFEMHHNINRFV	1972
	: ** : *::*:** * : .*** :*::** : * : * : * : * : *		
		ITAM	DOCK motif
hCLASP4	FEAPYTLSGKKQGCIEEQCKRRTILTTSNSF	YVKHRIPINCEQQINLKPIDGATDEIKD	1859
hCLASP5	YTPFTLEGRPRGELHEQYRRNTVLTMMHAF	YIKTRISVIQKEEFVLTPIEVAIEDMKK	1870
hCLASP3	YCTPFTLDGRAHGEHQFRKRTILTTSHAF	YIKTRVNVTHKEEILTPIEVAIEDMQK	1992
hCLASP2	FEMPFTQTGKRQGGVEEQCKRRTILTAIHCF	FYVKHRIPVMYQHHTDLNPIEVAIDEMSK	1830
hCLASP7	FCTPFTPDGRAHGEHQHKKRKTLLSTDHAF	YIKTRIRVCHREETVLTPEVAIEDMQK	1911
hCLASP1	FETPFTLSGKKHGGVAEQCKRRTILTTSHLF	FYVKHRIQVISQSSTELNPIEVAIDEMSR	2032
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	Coiled-coil		
hCLASP4	KTAELQKLCSSSTDVDMIQLQLKLC	QWVSQVQVNAAGPLAYARAFLNDSQASKYPPKKVSELK	1919
hCLASP5	KTQLQAVAINQEPDDAKMLQMVLC	QSVGATVNOGPLEVAQVFLAEIPADPKLYRHHNKLK	1930
hCLASP3	KTQLQELAFATHQDPPADPKMLQMVLC	QSVGTTVNOGPLEVAQVFLSEIPSDPKLFRHHNKLK	2052
hCLASP2	KVAELRQLCSSAEVDMIKLQLKLC	QSVSQQVNAAGPLAYARAFLLDNTNKRYPDNKVKLLK	1890
hCLASP7	KTRELAFAEQDPPDAKMLQMVLC	QSVGPTVNOGPLEVAQVFLAEIPEDPKLFRHHNKLK	1971
hCLASP1	KVSELNQLCTMEEVDMISLQLKLC	QSVSVKVNAGPMAYARAFLEETNAKKYPDNQVKLLK	2092
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	Coiled-coil		
hCLASP4	DMFRKFQACSALELNERLIKEDQVEYHEGLKS	NFRDMVKELSDIHEQILQEDTMHSP	1979
hCLASP5	LCFKEFIMRCGLAVEKNKRLITADQREYQ	QELKKYNKLNKLENLRPMIERKIPELYKPIFR	1990
hCLASP3	LCFKDFTKRCEDALRNKNSLIGPVQKEYQ	RELGLKSSP-----	2090
hCLASP2	EVFRQFVEACGOALAVNERLIKEDQLEYQ	EEMKANYREMAKELSEIMHEQICPLEEKTS-	1949
hCLASP7	LCFKDFCKKCEDALRNKALIGPDQKEYH	RELERNYCRLREALQPILTQRLPQLMAPTP-	2030
hCLASP1	EIFRQFADACGOALDVNERLIKEDQLEYQ	EELRSHYKMDLSELSTVMNEQITGRDDLSKR	2152
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	PDZ ligand		
hCLASP4	WMSNTLHVFCASISGTSSDRGYGSP	YAEV--	2008
hCLASP5	VESQKRDSFHRSSFRCETQLSQGS	-----	2015
hCLASP3	-----		
hCLASP2	VLPNSLHIFNAISGTPSTMTVMHG	MTSSSSVV	1980
hCLASP7	--PGLRNSLNRASFRKADL	-----	2047
hCLASP1	GVDQCTRVISKATPALPTVIS	SSAEV--	2180